

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: STROMINGER, JACK L.
WUCHERPFENNIG, KAI
- (ii) TITLE OF INVENTION: IDENTIFICATION OF SELF AND NON-SELF
ANTIGENS IMPLICATED IN AUTOIMMUNE DISEASE
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
(B) STREET: 600 ATLANTIC AVENUE
(C) CITY: BOSTON
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02210
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: TWOMEY, MICHAEL J.
(B) REGISTRATION NUMBER: 38,349
(C) REFERENCE/DOCKET NUMBER: H0498/7015
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-720-3500
(B) TELEFAX: 617-720-2441

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:
(A) ORGANISM: HOMO SAPIENS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Thr Gln Lys Ile Thr Tyr Arg Ile Ser Gly Val Gly Ile Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:
(A) ORGANISM: HOMO SAPIENS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe Gly Ile Phe Val Val Asp Lys Asn Thr Gly Asp Ile Asn Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Asn Ser Lys Ile Ala Phe Lys Ile Val Ser Gln Glu Pro Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Pro Met Phe Leu Leu Ser Arg Asn Thr Gly Glu Val Arg Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(iii) HYPOTHETICAL: NO

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Gln Ser Gly Thr Met Arg Thr Arg His Ser Thr Gly Gly Thr Asn
1 5 10 15

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: HERPES SIMPLEX

Phe Arg Gln Leu Val His Phe Val Arg Asp Phe Ala Gln Leu Leu
1 5 10 15

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

1. Name of the person		2. Date of birth		3. Place of birth		4. Nationality		5. Occupation		6. Address		7. Telephone number		8. Signature	
1.1	1.2	2.1	2.2	3.1	3.2	4.1	4.2	5.1	5.2	6.1	6.2	7.1	7.2	8.1	8.2
1.3	1.4	2.3	2.4	3.3	3.4	4.3	4.4	5.3	5.4	6.3	6.4	7.3	7.4	8.3	8.4
1.5	1.6	2.5	2.6	3.5	3.6	4.5	4.6	5.5	5.6	6.5	6.6	7.5	7.6	8.5	8.6
1.7	1.8	2.7	2.8	3.7	3.8	4.7	4.8	5.7	5.8	6.7	6.8	7.7	7.8	8.7	8.8
1.9	1.10	2.9	2.10	3.9	3.10	4.9	4.10	5.9	5.10	6.9	6.10	7.9	7.10	8.9	8.10
1.11	1.12	2.11	2.12	3.11	3.12	4.11	4.12	5.11	5.12	6.11	6.12	7.11	7.12	8.11	8.12
1.13	1.14	2.13	2.14	3.13	3.14	4.13	4.14	5.13	5.14	6.13	6.14	7.13	7.14	8.13	8.14
1.15	1.16	2.15	2.16	3.15	3.16	4.15	4.16	5.15	5.16	6.15	6.16	7.15	7.16	8.15	8.16
1.17	1.18	2.17	2.18	3.17	3.18	4.17	4.18	5.17	5.18	6.17	6.18	7.17	7.18	8.17	8.18
1.19	1.20	2.19	2.20	3.19	3.20	4.19	4.20	5.19	5.20	6.19	6.20	7.19	7.20	8.19	8.20
1.21	1.22	2.21	2.22	3.21	3.22	4.21	4.22	5.21	5.22	6.21	6.22	7.21	7.22	8.21	8.22
1.23	1.24	2.23	2.24	3.23	3.24	4.23	4.24	5.23	5.24	6.23	6.24	7.23	7.24	8.23	8.24
1.25	1.26	2.25	2.26	3.25	3.26	4.25	4.26	5.25	5.26	6.25	6.26	7.25	7.26	8.25	8.26
1.27	1.28	2.27	2.28	3.27	3.28	4.27	4.28	5.27	5.28	6.27	6.28	7.27	7.28	8.27	8.28
1.29	1.30	2.29	2.30	3.29	3.30	4.29	4.30	5.29	5.30	6.29	6.30	7.29	7.30	8.29	8.30
1.31	1.32	2.31	2.32	3.31	3.32	4.31	4.32	5.31	5.32	6.31	6.32	7.31	7.32	8.31	8.32
1.33	1.34	2.33	2.34	3.33	3.34	4.33	4.34	5.33	5.34	6.33	6.34	7.33	7.34	8.33	8.34
1.35	1.36	2.35	2.36	3.35	3.36	4.35	4.36	5.35	5.36	6.35	6.36	7.35	7.36	8.35	8.36
1.37	1.38	2.37	2.38	3.37	3.38	4.37	4.38	5.37	5.38	6.37	6.38	7.37	7.38	8.37	8.38
1.39	1.40	2.39	2.40	3.39	3.40	4.39	4.40	5.39	5.40	6.39	6.40	7.39	7.40	8.39	8.40
1.41	1.42	2.41	2.42	3.41	3.42	4.41	4.42	5.41	5.42	6.41	6.42	7.41	7.42	8.41	8.42
1.43	1.44	2.43	2.44	3.43	3.44	4.43	4.44	5.43	5.44	6.43	6.44	7.43	7.44	8.43	8.44
1.45	1.46	2.45	2.46	3.45	3.46	4.45	4.46	5.45	5.46	6.45	6.46	7.45	7.46	8.45	8.46
1.47	1.48	2.47	2.48	3.47	3.48	4.47	4.48	5.47	5.48	6.47	6.48	7.47	7.48	8.47	8.48
1.49	1.50	2.49													

(A) ORGANISM: ADENOVIRUS TYPE 12

Asp Phe Glu Val Val Thr Phe Leu Lys Asp Val Leu Pro Glu Phe
1 5 10 15

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

(A) ORGANISM: PSEUDOMONAS AERUGINOSA

Asp Arg Leu Leu Met / Leu Phe Ala Lys Asp Val Val Ser Arg Asn
1 5 10 15

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

(A) ORGANISM: HUMAN PAPILLOMAVIRUS TYPE 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ile Gly Gly Arg Val His Phe Phe Lys Asp Ile Ser Pro Ile Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: EPSTEIN-BARR VIRUS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Gly Gly Val Tyr His Phe Val Lys Lys His Val His Glu Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: INFLUENZA VIRUS TYPE A

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Tyr Arg Asn Leu Val Trp Phe Ile Lys Lys Asn Thr Arg Tyr Pro
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: REOVIRUS TYPE 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Arg Ala Ala Phe Leu Phe Lys Thr Val Gly Phe Gly Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HERPES SIMPLEX VIRUS

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Gly Gly Arg Arg Leu Phe Phe Val Lys Ala His Val Arg Glu Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HOMO SAPIENS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg
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